

#6

034100-003.ST25

SEQUENCE LISTING

<110> Taniguchi, Naoyuki
Miyoshi, Eiichi
Saito, Takeshi

<120> Glycosyltransferase GnT-V Having Neovascularization Action

<130> 034100-003

<140> US 10/500,841
<141> 2004-07-07

<150> PCT/JP02/13879
<151> 2002-12-27

<150> JP 2002-2056
<151> 2002-01-09

<160> 13

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 5
<212> PRT
<213> Homo sapiens

<400> 1
Thr Pro Trp Gly Lys
1 5

<210> 2
<211> 6
<212> PRT
<213> Homo sapiens

<400> 2
Asn Ile Pro Ser Tyr Val
1 5

<210> 3
<211> 17
<212> PRT
<213> Homo sapiens

<400> 3
Val Leu Asp Ser Phe Gly Thr Glu Pro Glu Phe Asn His Ala Asn Tyr
1 5 10 15
Ala

<210> 4
<211> 6
<212> PRT
<213> Homo sapiens

<400> 4

Asp Leu Gln Phe Leu Leu
1 5

<210> 5

<211> 7

<212> PRT

<213> Homo sapiens

<400> 5

Asn Thr Asp Phe Phe Ile Gly
1 5

<210> 6

<211> 2095

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (156)...(2095)

<400> 6

```

ccggctgaag catcagaatg gaagtgagga aaggcaacca gctgacacag gagccagagt 60
gagaccagca gactctcaca ctcaacctac accatgaatt tgtgtctatc ttctacgcgt 120
taagagccaa ggacaggtga agttgccaga gagca atg gct ctc ttc act ccg 173
                               Met Ala Leu Phe Thr Pro
                               1 5

```

```

tgg aag ttg tcc tct cag aag ctg ggc ttt ttc ctg gtg act ttt ggc 221
Trp Lys Leu Ser Ser Gln Lys Leu Gly Phe Phe Leu Val Thr Phe Gly
                10                15                20

```

```

ttc att tgg ggt atg atg ctt ctg cac ttt acc atc cag cag cga act 269
Phe Ile Trp Gly Met Met Leu Leu His Phe Thr Ile Gln Gln Arg Thr
                25                30                35

```

```

cag cct gaa agc agc tcc atg ctg cgc gag cag atc ctg gac ctc agc 317
Gln Pro Glu Ser Ser Ser Met Leu Arg Glu Gln Ile Leu Asp Leu Ser
                40                45                50

```

```

aaa agg tac atc aag gca ctg gca gaa gaa aac agg aat gtg gtg gat 365
Lys Arg Tyr Ile Lys Ala Leu Ala Glu Glu Asn Arg Asn Val Val Asp
                55                60                65                70

```

```

ggg cca tac gct gga gtc atg aca gct tat gat ctg aag aaa acc ctt 413
Gly Pro Tyr Ala Gly Val Met Thr Ala Tyr Asp Leu Lys Lys Thr Leu
                75                80                85

```

```

gct gtg tta tta gat aac att ttg cag cgc att ggc aag ttg gag tcg 461
Ala Val Leu Leu Asp Asn Ile Leu Gln Arg Ile Gly Lys Leu Glu Ser
                90                95                100

```

```

aag gtg gac aat ctt gtt gtc aat ggc acc gga aca aac tca acc aac 509
Lys Val Asp Asn Leu Val Val Asn Gly Thr Gly Thr Asn Ser Thr Asn
                105                110                115

```

034100-003.ST25

tcc Ser	act Thr	aca Thr	gct Ala	gtt Val	ccc Pro	agc Ser	ttg Leu	gtt Val	gca Ala	ctt Leu	gag Glu	aaa Lys	att Ile	aat Asn	gtg Val	557
120						125					130					
gca Ala	gat Asp	atc Ile	att Ile	aac Asn	gga Gly	gct Ala	caa Gln	gaa Glu	aaa Lys	tgt Cys	gta Val	ttg Leu	cct Pro	cct Pro	atg Met	605
135					140					145					150	
gac Asp	ggc Gly	tac Tyr	cct Pro	cac His	tgt Cys	gag Glu	gga Gly	aag Lys	atc Ile	aag Lys	tgg Trp	atg Met	aaa Lys	gac Asp	atg Met	653
				155					160					165		
tgg Trp	cgt Arg	tca Ser	gat Asp	ccc Pro	tgc Cys	tac Tyr	gca Ala	gac Asp	tat Tyr	gga Gly	gtg Val	gat Asp	gga Gly	tcc Ser	acc Thr	701
			170					175					180			
tgc Cys	tct Ser	ttt Phe	ttt Phe	att Ile	tac Tyr	ctc Leu	agt Ser	gag Glu	gtt Val	gaa Glu	aat Asn	tgg Trp	tgt Cys	cct Pro	cat His	749
		185					190					195				
tta Leu	cct Pro	tgg Trp	aga Arg	gca Ala	aaa Lys	aat Asn	ccc Pro	tac Tyr	gaa Glu	gaa Glu	gct Ala	gat Asp	cat His	aat Asn	tca Ser	797
	200					205					210					
ttg Leu	gcg Ala	gaa Glu	att Ile	cgt Arg	aca Thr	gat Asp	ttt Phe	aat Asn	att Ile	ctc Leu	tac Tyr	agt Ser	atg Met	atg Met	aaa Lys	845
215					220					225					230	
aag Lys	cat His	gaa Glu	gaa Glu	ttc Phe	cgg Arg	tgg Trp	atg Met	aga Arg	cta Leu	cgg Arg	atc Ile	cgg Arg	cga Arg	atg Met	gct Ala	893
				235					240					245		
gac Asp	gca Ala	tgg Trp	atc Ile	caa Gln	gca Ala	atc Ile	aag Lys	tcc Ser	ctg Leu	gca Ala	gaa Glu	aag Lys	cag Gln	aac Asn	ctt Leu	941
			250					255					260			
gaa Glu	aag Lys	aga Arg	aag Lys	cgg Arg	aag Lys	aaa Lys	gtc Val	ctc Leu	gtt Val	cac His	ctg Leu	gga Gly	ctc Leu	ctg Leu	acc Thr	989
		265					270					275				
aag Lys	gaa Glu	tct Ser	gga Gly	ttt Phe	aag Lys	att Ile	gca Ala	gag Glu	aca Thr	gct Ala	ttc Phe	agt Ser	ggg Gly	ggc Gly	cct Pro	1037
	280					285					290					
ctt Leu	ggt Gly	gaa Glu	tta Leu	gtt Val	caa Gln	tgg Trp	agt Ser	gat Asp	tta Leu	att Ile	aca Thr	tct Ser	ctg Leu	tac Tyr	tta Leu	1085
295					300					305					310	
ctg Leu	ggc Gly	cat His	gac Asp	att Ile	agg Arg	att Ile	tca Ser	gct Ala	tca Ser	ctg Leu	gct Ala	gag Glu	ctc Leu	aag Lys	gaa Glu	1133
			315					320						325		
atc Ile	atg Met	aag Lys	aag Lys	gtt Val	gta Val	gga Gly	aac Asn	cga Arg	tct Ser	ggc Gly	tgc Cys	cca Pro	act Thr	gta Val	gga Gly	1181
			330				335						340			
gac Asp	aga Arg	att Ile	gtt Val	gag Glu	ctc Leu	att Ile	tac Tyr	att Ile	gat Asp	att Ile	gta Val	gga Gly	ctt Leu	gct Ala	caa Gln	1229
		345					350					355				

ttc aag aaa act ctt gga cca tcc tgg gtt cat tac cag tgc atg ctc	1277
Phe Lys Lys Thr Leu Gly Pro Ser Trp Val His Tyr Gln Cys Met Leu	
360 365 370	
cga gtc ctt gat tca ttt ggt act gaa ccc gaa ttt aat cat gca aat	1325
Arg Val Leu Asp Ser Phe Gly Thr Glu Pro Glu Phe Asn His Ala Asn	
375 380 385 390	
tat gcc caa tcg aaa ggc cac aag acc cct tgg gga aaa tgg aat ctg	1373
Tyr Ala Gln Ser Lys Gly His Lys Thr Pro Trp Gly Lys Trp Asn Leu	
395 400 405	
aac cct cag cag ttt tat acc atg ttc cct cat acc cca gac aac agc	1421
Asn Pro Gln Gln Phe Tyr Thr Met Phe Pro His Thr Pro Asp Asn Ser	
410 415 420	
ttt ctg ggg ttt gtg gtt gag cag cac ctg aac tcc agt gat atc cac	1469
Phe Leu Gly Phe Val Val Glu Gln His Leu Asn Ser Ser Asp Ile His	
425 430 435	
cac att aat gaa atc aaa agg cag aac cag tcc ctt gtg tat ggc aaa	1517
His Ile Asn Glu Ile Lys Arg Gln Asn Gln Ser Leu Val Tyr Gly Lys	
440 445 450	
gtg gat agc ttc tgg aag aat aag aag atc tac ttg gac att att cac	1565
Val Asp Ser Phe Trp Lys Asn Lys Lys Ile Tyr Leu Asp Ile Ile His	
455 460 465 470	
aca tac atg gaa gtg cat gca act gtt tat ggc tcc agc aca aag aat	1613
Thr Tyr Met Glu Val His Ala Thr Val Tyr Gly Ser Ser Thr Lys Asn	
475 480 485	
att ccc agt tac gtg aaa aac cat ggt atc ctc agt gga cgg gac ctg	1661
Ile Pro Ser Tyr Val Lys Asn His Gly Ile Leu Ser Gly Arg Asp Leu	
490 495 500	
cag ttc ctt ctt cga gaa acc aag ttg ttt gtt gga ctt ggg ttc cct	1709
Gln Phe Leu Leu Arg Glu Thr Lys Leu Phe Val Gly Leu Gly Phe Pro	
505 510 515	
tac gag ggc cca gct ccc ctg gaa gct atc gca aat gga tgt gct ttt	1757
Tyr Glu Gly Pro Ala Pro Leu Glu Ala Ile Ala Asn Gly Cys Ala Phe	
520 525 530	
ctg aat ccc aag ttc aac cca ccc aaa agc agc aaa aac aca gac ttt	1805
Leu Asn Pro Lys Phe Asn Pro Pro Lys Ser Ser Lys Asn Thr Asp Phe	
535 540 545 550	
ttc att ggc aag cca act ctg aga gag ctg aca tcc cag cat cct tac	1853
Phe Ile Gly Lys Pro Thr Leu Arg Glu Leu Thr Ser Gln His Pro Tyr	
555 560 565	
gct gaa gtt ttc atc ggg cgg cca cat gtg tgg act gtt gac ctc aac	1901
Ala Glu Val Phe Ile Gly Arg Pro His Val Trp Thr Val Asp Leu Asn	
570 575 580	
aat cag gag gaa gta gag gat gca gtg aaa gca att tta aat cag aag	1949
Asn Gln Glu Glu Val Glu Asp Ala Val Lys Ala Ile Leu Asn Gln Lys	

034100-003.ST25

585	590	595	
att gag cca tac atg cca tat gaa ttt acg tgc gag ggg atg cta cag			1997
Ile Glu Pro Tyr Met Pro Tyr Glu Phe Thr Cys Glu Gly Met Leu Gln			
600	605	610	
aga atc aat gct ttc att gaa aaa cag gac ttc tgc cat ggg caa gtg			2045
Arg Ile Asn Ala Phe Ile Glu Lys Gln Asp Phe Cys His Gly Gln Val			
615	620	625	630
atg tgg cca ccc ctc agc gcc cta cag gtc aag ctt gct gag ccc ggg			2093
Met Trp Pro Pro Leu Ser Ala Leu Gln Val Lys Leu Ala Glu Pro Gly			
	635	640	645
cc			2095
<210> 7			
<211> 16			
<212> PRT			
<213> Homo sapiens			
<400> 7			
Lys Ser Leu Ala Glu Lys Gln Asn Leu Glu Lys Arg Lys Arg Lys Lys			
1	5	10	15
<210> 8			
<211> 24			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> compound suppressing expression			
<400> 8			
gggagtgagg atgatgtagg gaag			24
<210> 9			
<211> 24			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> compound suppressing expression			
<400> 9			
atggggcaga ggaacttacg ttat			24
<210> 10			
<211> 6			
<212> PRT			
<213> Homo sapiens			
<400> 10			
Gly Arg Gly Lys Arg Arg			
1	5		
<210> 11			

<211> 6
<212> PRT
<213> Homo sapiens

<400> 11
Lys Arg Lys Arg Lys Lys
1 5

<210> 12
<211> 6
<212> PRT
<213> Homo sapiens

<400> 12
Phe Ser Gly Gly Pro Leu
1 5

<210> 13
<211> 5
<212> PRT
<213> Homo sapiens

<400> 13
His Phe Thr Ile Gln
1 5